1.4 kb—

Figure 1

```
   1   CCCTTCTCCAGGGACTCTGGCTGCCAGCAGCTCCGCCTTTCAGATCAATTCTCGACCACC    60

  61   CACCTTGGGACTGCCGCCCAGTCCTGCCCTCTGGATCAGTGGGGTCCAGACACGCCCCCT   120

 121   CCAGGACCTCAAAGCACCCCCGACCTAAGGTCACCAGCCCACTGGCCCCAGACGCAGTGG   180

 181   GCTCCGCTGACTCTCTTGGACACCTCCTGGGAGGAAAATGCTCCCTGTCTGCCATCGTTT   240
                                             M  L  P  V  C  H  R  F

 241   TTGCGACCACCTCCTCCTCCTGCTCTTGCTGCCCTCGACGACCCTGGCCCCCGCGCCAGC   300
         C  D  H  L  L  L  L  L  L  L  P  S  T  T  L  A  P  A  P  A

 301   ATCCATGGGCCCCGCTGCCGCCCTGCTCCAGGTTCTTGGGCTTCCCGAAGCGCCCCGGAG   360
         S  M  G  P  A  A  A  L  L  Q  V  L  G  L  P  E  A  P  R  S

 361   CGTCCCCACACACCGACCTGTGCCTCCTGTCATGTGGCGCCTATTCCGTCGCCGTGACCC   420
         V  P  T  H  R  P  V  P  P  V  M  W  R  L  F  R  R  R  D  P

 421   CCAGGAGGCCAGAGTGGGACGCCCTCTGCGGCCATGCCACGTGGAGGAACTAGGGGTCGC   480
         Q  E  A  R  V  G  R  P  L  R  P  C  H  V  E  E  L  G  V  A

 481   CGGAAACATTGTGCGCCACATCCCCGACAGCGGTCTGTCCTCCAGGCCCGCACAACCCGC   540
         G  N  I  V  R  H  I  P  D  S  G  L  S  S  R  P  A  Q  P  A

 541   CAGGACCTCGGGGCTGTGCCCCGAGTGGACAGTCGTCTTTGACCTGTCGAATGTGGAGCC   600
         R  T  S  G  L  C  P  E  W  T  V  V  F  D  L  S  N  V  E  P

 601   CACAGAGCGCCCAACACGCGCGCGCTTAGAGTTGCGGCTGGAGGCTGAGTGTGAAGATAC   660
         T  E  R  P  T  R  A  R  L  E  L  R  L  E  A  E  C  E  D  T

 661   AGGAGGGTGGGAGCTAAGCGTGGCACTGTGGGCCGACGCAGAGCATCCAGGGCCTGAGCT   720
         G  G  W  E  L  S  V  A  L  W  A  D  A  E  H  P  G  P  E  L

 721   GCTGCGCGTGCCGGCGCCACCAGGGGTGCTCCTGCGCGCAGACCTACTGGGGACTGCAGT   780
         L  R  V  P  A  P  P  G  V  L  L  R  A  D  L  L  G  T  A  V

 781   AGCCGCCAACGCATCAGTGCCCTGTACTGTGCGCCTGGCGCTGTCACTGCACCCTGGGGC   840
         A  A  N  A  S  V  P  C  T  V  R  L  A  L  S  L  H  P  G  A

 841   CACTGCAGCCTGTGGGCGCCTGGCTGAGGCCTCCCTGCTGCTGGTGACGCTGGACCCACG   900
         T  A  A  C  G  R  L  A  E  A  S  L  L  L  V  T  L  D  P  R

 901   CCTGTGTCCCTTGCCGCGATTGCGGCGCCACACGGAGCCCAGGGTAGAAGTTGGTCCAGT   960
         L  C  P  L  P  R  L  R  R  H  T  E  P  R  V  E  V  G  P  V

 961   GGGCACTTGTCGTACCCGACGGTTGCATGTGAGCTTCCGTGAGGTGGGCTGGCACCGTTG  1020
         G  T  C  R  T  R  R  L  H  V  S  F  R  E  V  G  W  H  R  W

1021   GGTGATCGCGCCGCGTGGCTTCCTAGCCAACTTCTGCCAGGGCACGTGCGCACTACCCGA  1080
         V  I  A  P  R  G  F  L  A  N  F  C  Q  G  T  C  A  L  P  E

1081   AACGCTGAGGGGACCCGGCGGGCCGCCTGCACTCAACCACGCTGTGCTGCGCGCGCTCAT  1140
         T  L  R  G  P  G  G  P  P  A  L  N  H  A  V  L  R  A  L  M

1141   GCACGCAGCTGCTCCCACCCCGGGTGCAGGCTCGCCCTGCTGCGTGCCAGAGCGTCTATC  1200
         H  A  A  A  P  T  P  G  A  G  S  P  C  C  V  P  E  R  L  S

1201   ACCCATCTCCGTGCTCTTCTTCGACAATAGTGACAACGTGGTCCTGCGACACTACGAAGA  1260
         P  I  S  V  L  F  F  D  N  S  D  N  V  V  L  R  H  Y  E  D

1261   CATGGTGGTGGATGAGTGTGGCTGCCGTTGACCACCCGGGACACCCTTTCAGGGACCGCC  1320
         M  V  V  D  E  C  G  C  R

1321   CCACGCAAAAGCAGGGACTGTTTGTTCATGTTTTATTGGTGACAAAAAGCTTAAAACAAA  1380

1381   TTTGACT   1387
```

GDF-1   RRHTEPRVEVG--PVGT QRTRRLHVSF -REVGWHRWVIAPRGFLANF QGT ALPETLRGPGGPP

Vg-1   RKRSYSKLPFT--ASNI KKRHLYVEF -KDVGWQNVIAPQGYMANY YGE P-YPLTEILNG--
Vgr-1   GSGSSDYNGSE--LKTA KKHELYVSF -QDLGWQDWIIAPKGYAANY DGE P-SFPLNAHMNA--
BMP-2a   KRQAKHKQRKR--LKSS KRHPLYVDF -SDVGWNDWIVAPPGYHAFY HGD P-FPLADHLNS--
BMP-2b   SPKHHSQRARK--KNKN RRHSLYVDF -SDVGWNDWIVAPPGYQAFY HGD P-FPLADHLNS--
BMP-3   TLKKARRKQWI--EPRN ARRYLKVDE -ADIGWSEWIISPKSFDAYY SGA QFPMPKSLKPS--
DPP   -HARRPTRRKN--HDDT RRHSLYVDF -SDVGWDDWIVAPLGYDAYY HGK P-FPLADHFNS--
MIS   GRAQRSAGATA--ADGP ALRELSVDLRAE---RSVLIPETYQANN HGV GWPQSDRNPRY--
Inhibin α RLLQRPPEEPA--AHAN HRVALNISF-QELGWERWIVYPPSFIFHY HGG GLHIPPNLSLPV-
Inhibin βA GLE---CDGKV--NIC KKQFFVSF-KDIGWNDWIIAPSGYHANY EGE PSHIAGTSGSSL-
Inhibin βB GLE---CDGRT--NLC RQQFIDF-RLIGWNDWIIAPTGYYGNY EGS PAYLAGVPGSAS-
TGF-β1   ALDTNYCFSST--EKNC VRQ-LYIDFRKDLGWK-WIHEPKGYHANF LGP P-YIW----SLD-
TGF-β2   ALDAAYCFRNV--QDNC LRP-LYIDFKRDLGWK-WIHEPKGYNANF AGA P-YLW----SSD-
TGF-β3   ALDTNYCFRNL--EENC VRP-LYIDFERQDLGWK-WVHEPKGYYANE SGP P-YLR----SAD-
TGF-β4   DLDTDYCFGPGTDEKNC VRP-LYIDFERKDLQWK-WIHEPKGYMANF MGP P-YIW----SAD-
TGF-β5   GVGQEYCFGNN--GPNC VKP-LYINFRKDLGWK-WIHEPKGYEANY LGN P-YIW----SMD-

GDF-1   ALNHAVLRALMHAAA-PTPGAGSPCCV--PERLSPISVLFF-DNSDNVVLRHYEDMVVDE GGR

Vg-1   -SNHAILQTLVHS--IEPEDIPLPCCV--PTKMSPISMLFY-DNNDNVVLRHYENMAVDE C GCR
Vgr-1   -TNHAIVQTLVHL--MNPEYVPKPCCA--PTKLNAISVLYF-DDNSNVILKKYRNMVVRA C GCH
BMP-2a   -TNHAIVQTLVNS--VNSKIPKACCV--PTELSAISMLYL-DENEKVVLKNYQDMVVEG C GCR
BMP-2b   -TNHAIVQTLVNS--VNSSIPKACCV--PTELSAISMLYL-DEYDKVVLKNYQEMVVEG C GCR
BMP-3   -NHATIQSIVRA--VGVVPGIPEPCCV--PEKMSSLSILFF-DENKNVVLKVYPNMTVES C ACR
DPP   -TNHAVVQTLVNN--MNPGKVPKACCV--PTQLDSVAMLYLND-QSTVVLKNYQEMTVVG C GCR
MIS   -GNH-VVLL-KMQARGAALARPPCCV--PTAYAGKLLISLSEER---ISAHHVPNMVATE C GCR
Inhibin α -PGAPPT----PAQPYSLLPGAQPCCAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQH C ACI
Inhibin βA -SFHSTVINHYRMRGHSPFANLKSCCV--PTKLRPMSMLYY-DDGQNIIKKDIQNMIVEE C GCS
Inhibin βB -SFHTAVVNQYRMRGLNPGT-VNSCCI--PTKLSTMSMLYF-DDEYNIVKRDVPNMIVEE C GCA
TGF-β1   -TQYSKVLALYN--QHNPGASAAPCCV--PQALEPLPIVYY-VGRKPKV-EQLSNMIVKS C KCS
TGF-β2   -TQHSRVLSLYN--TINPEASASPCCV--SQDLEPLTILYY-IGKTPKI-EQLSNMIVKS C KCS
TGF-β3   -TTHSTVLGLYN--TLNPEASASPCCV--PQDLEPLTILYY-VGRTPKV-EQLSNMVVRA C KCS
TGF-β4   -TQYTKVLALYN--QHNPGASAAPCCV--PQTLDPLPIIYY-VGRNVRV-EQLSNMVVRA C KCS
TGF-β5   -TQYSKVLSLYN--QNNPGASISPCCV--PDVLEPLPIIYY-VGRTAKV-EQLSNMVVRS C NCS

Figure 3a

	GDF-1	Vg-1	Vgr-1	BMP-2a	BMP-2b	BMP-3	DPP	MIS	Inhibin α	Inhibin βA	Inhibin βB	TGF-β1	TGF-β2	TGF-β3	TGF-β4	TGF-β5
GDF-1	100	52	40	38	39	41	34	33	22	31	31	26	27	30	26	26
Vg-1	–	100	59	59	57	45	49	27	23	45	40	34	35	38	33	35
Vgr-1	–	–	100	62	59	43	57	26	23	45	39	35	37	38	37	37
BMP-2a	–	–	–	100	92	44	73	26	20	42	37	34	34	35	33	33
BMP-2b	–	–	–	–	100	44	74	27	21	41	37	33	34	35	33	33
BMP-3	–	–	–	–	–	100	42	25	28	33	33	29	31	31	26	28
DPP	–	–	–	–	–	–	100	25	20	39	36	35	35	35	35	34
MIS	–	–	–	–	–	–	–	100	18	22	22	24	21	26	25	24
Inhibin α	–	–	–	–	–	–	–	–	100	23	21	24	23	24	24	24
Inhibin βA	–	–	–	–	–	–	–	–	–	100	63	38	37	36	35	38
Inhibin βB	–	–	–	–	–	–	–	–	–	–	100	35	35	36	34	32
TGF-β1	–	–	–	–	–	–	–	–	–	–	–	100	73	77	85	81
TGF-β2	–	–	–	–	–	–	–	–	–	–	–	–	100	81	68	69
TGF-β3	–	–	–	–	–	–	–	–	–	–	–	–	–	100	74	73
TGF-β4	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100	78
TGF-β5	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100

Figure 36

GDF-1 54 PVPPVMWRLFRRRDPQEARVGRPLRPCHVEELGVAGNIVRHIPDSGLSSRPAQPARTSGLCPEWTVVFDLSNVEPTERPT 133

Vg-1   46 PVPSILWRIFNQRMGSSIQKKKPDL CFVEEFNVPGSVIRVFPDQGRFIIPYSDDIHPTQCLEKRLFFNISAIEKEERVT 124

GDF-1 219 SLLLVTLDPRLCPLPR 234
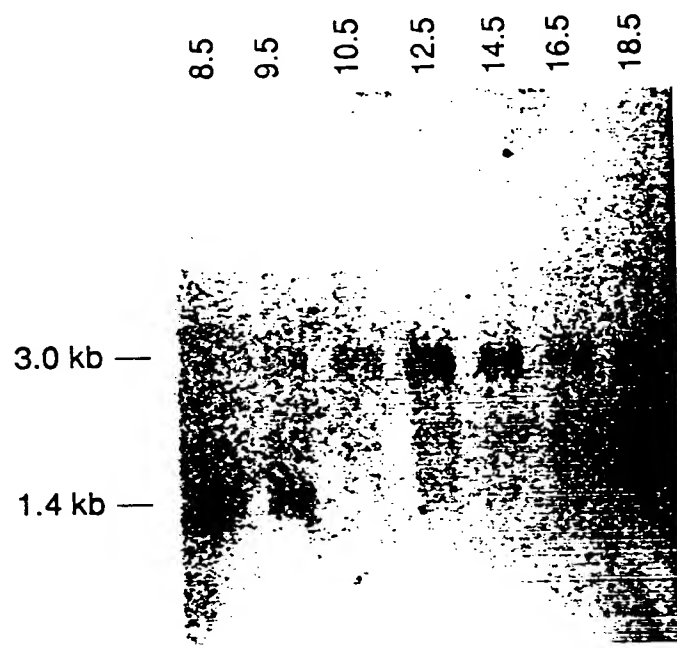
Vg-1   228 SLLTVTLNPLRCKRPR 243

Figure 4

Hamster   Mouse   Human

E   B   H   E   B   H   E   B   H

8.1
7.1
6.1
5.1
4.1

3.1

2.0

1.0

0.5

Figure 5

8.5 9.5 10.5 12.5 14.5 16.5 18.5

3.0 kb —

1.4 kb —
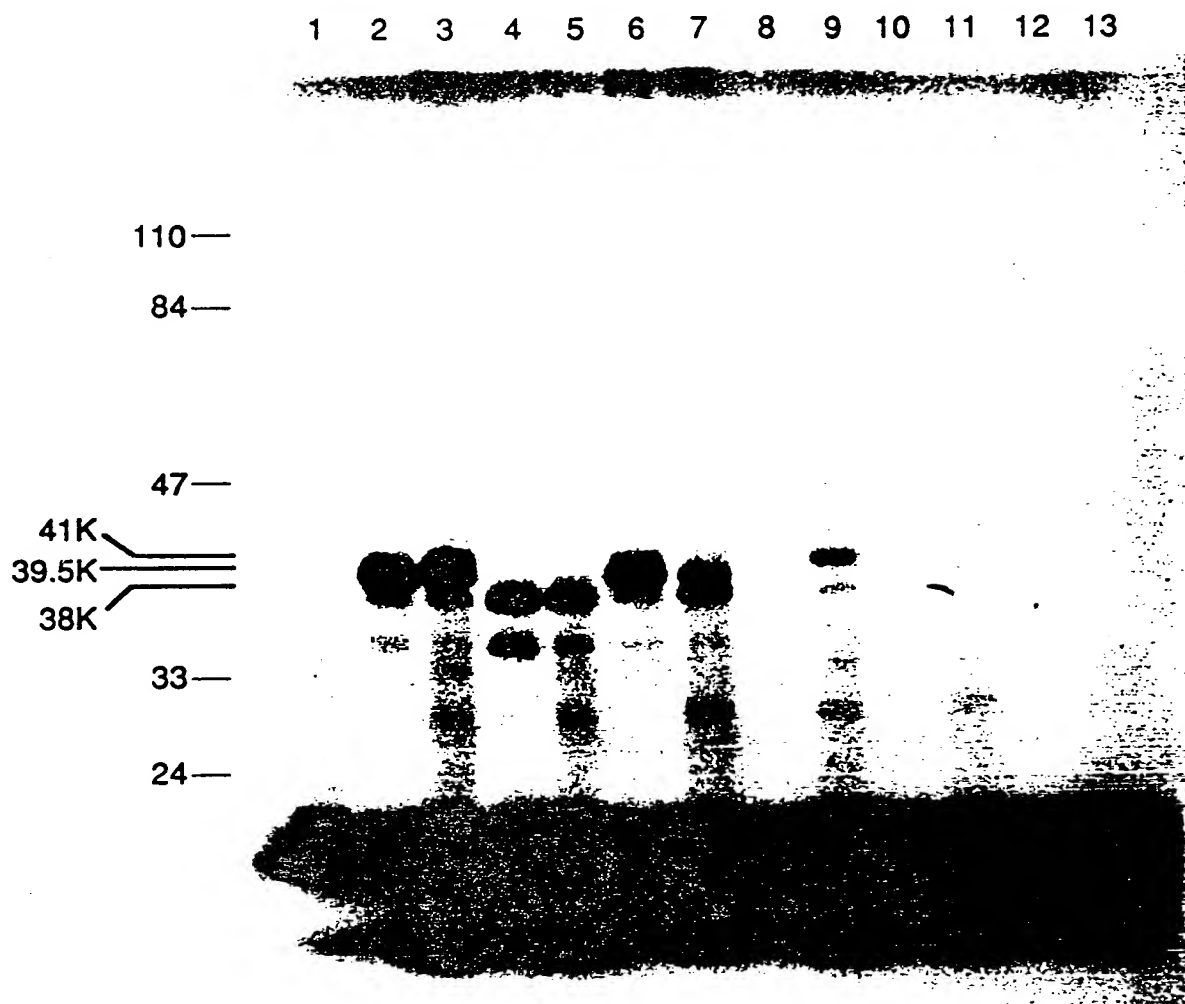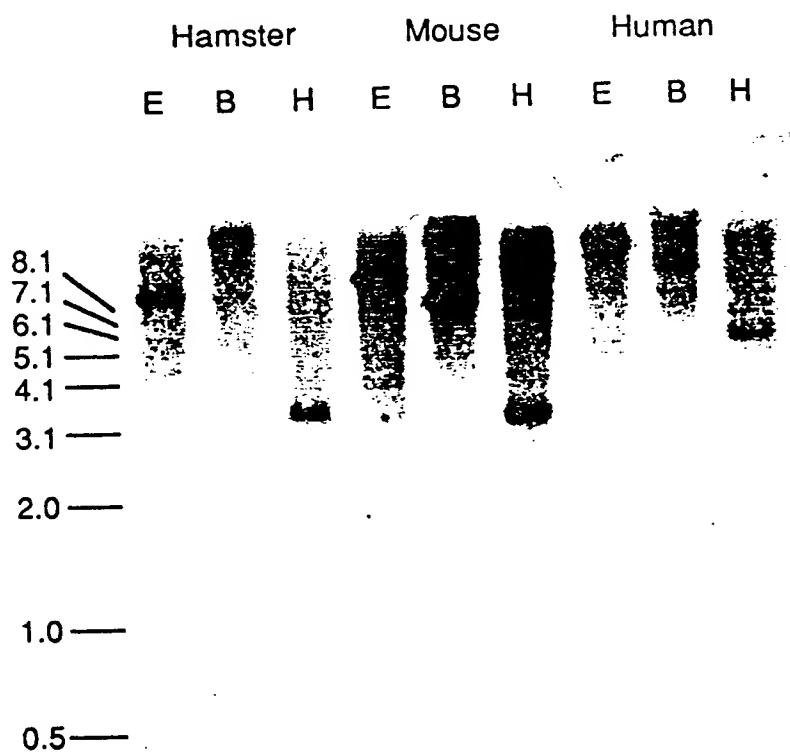
Figure 6

3.0 kb —

10.5 d placenta
testis
seminal vesicle
ovary
oviduct
uterus
brain
thymus
heart
lung
kidney
adrenal
spleen
liver
intestine
pancreas

Figure 7

whole brain

14 day embryonic
16 day embryonic
18 day embryonic
2 day post-natal
7 day post-natal
adult
spinal cord
cerebellum
brain stem

3.0 kb —
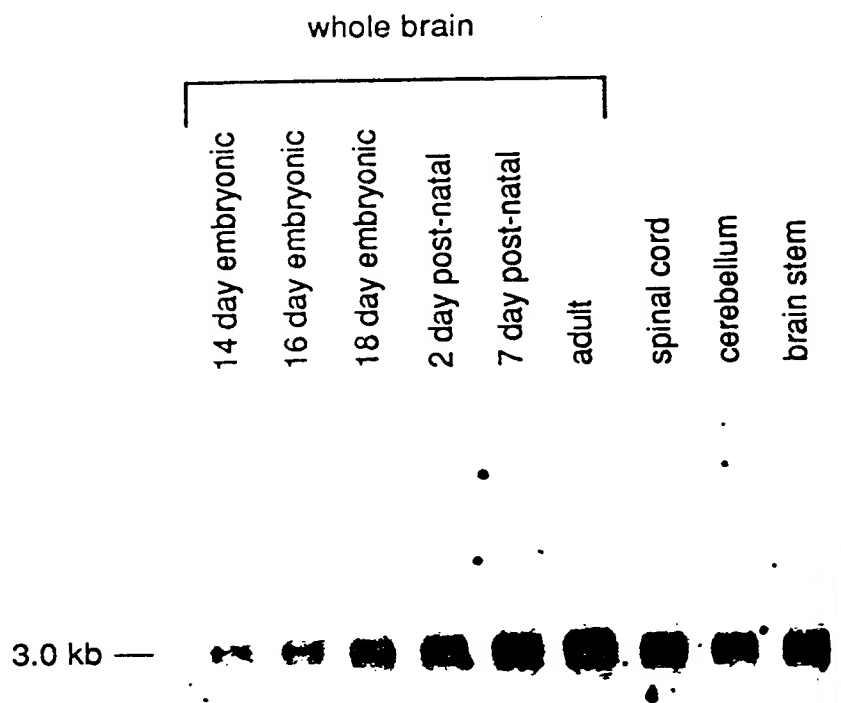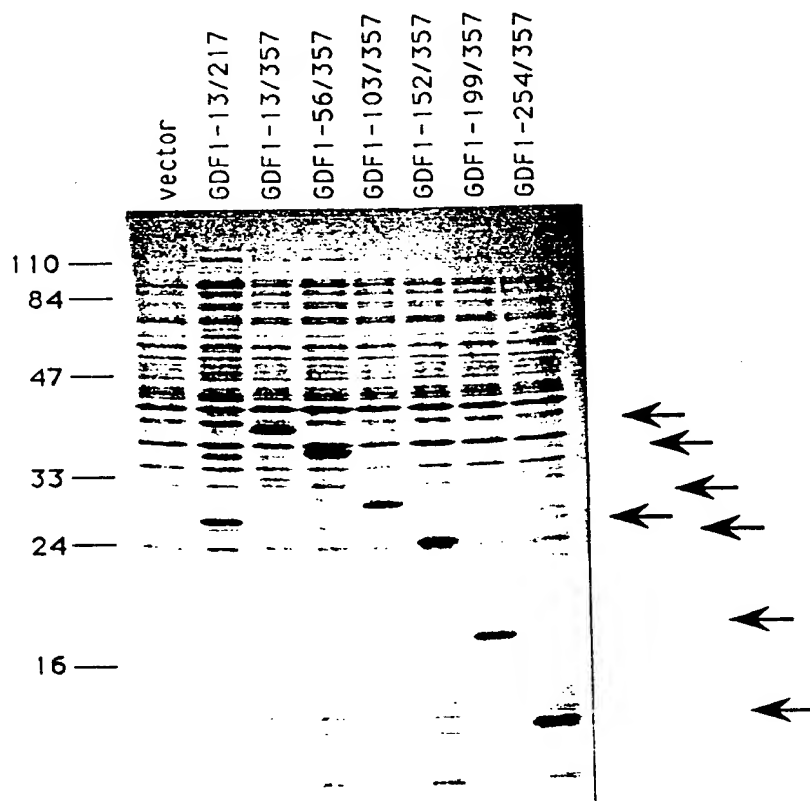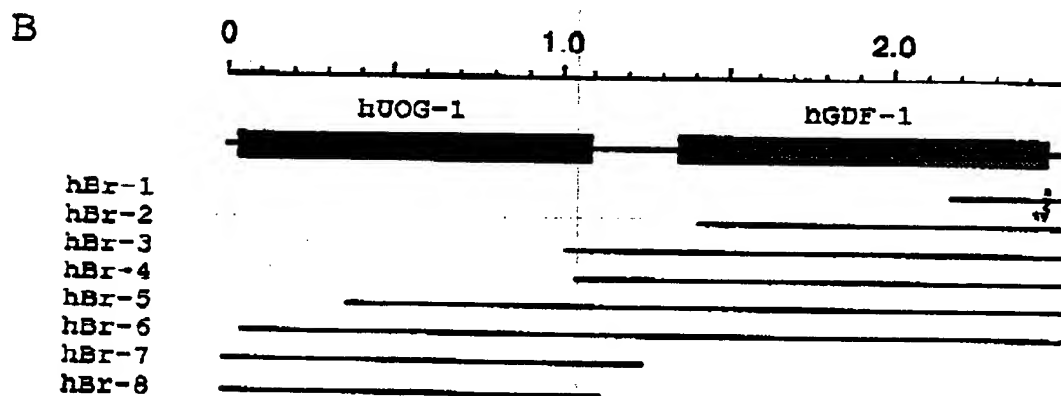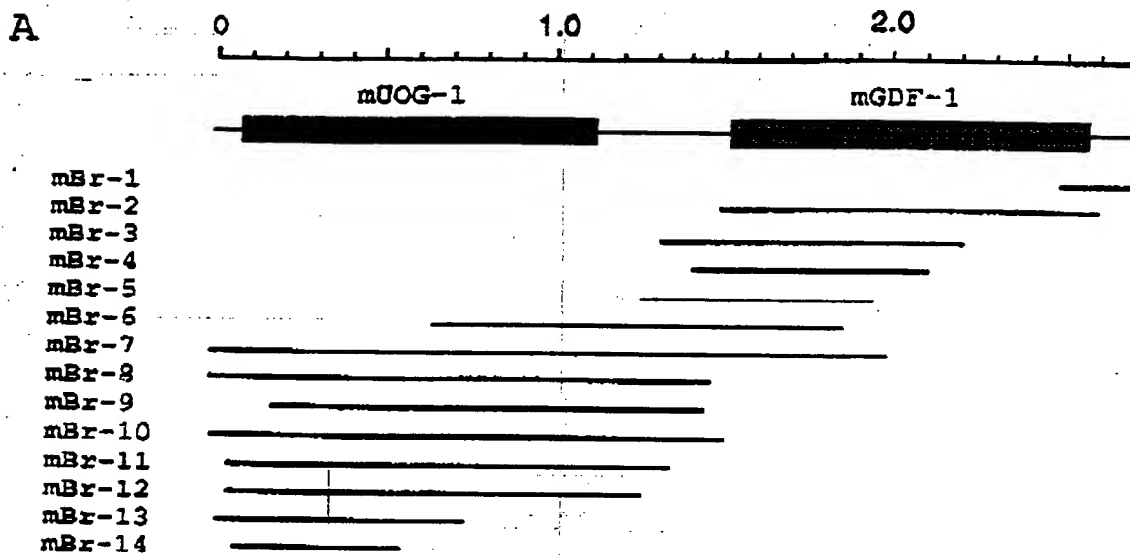
Figure 8

Figure 9

Figure 10

```
  1  GCGCGTGACGCGAGGGCGCGCGGCGACTCGGACCGGTGCAGGCAACAGCGGAGACAGCGG    60
 61  AGAATTGGATAGCATGGCTGCTGCCGCGGCGACCCCCAGGCTCGAGGCGCCAGAGCCCAT   120
         M  A  A  A  A  A  T  P  R  L  E  A  P  E  P  M
121  GCCGAGTTATGCGCAGATGTTGCAACGAAGCTGGGCCTCGGCGCTGGCGGCGGCTCAGGG   180
      P  S  Y  A  Q  M  L  Q  R  S  W  A  S  A  L  A  A  A  Q  G
181  CTGCGGGGACTGCGGCTGGGGACTGGCGCGCCGCCGCCTGGCGGAGCACGCGCACCTGGC   240
      C  G  D  C  G  W  G  L  A  R  R  G  L  A  E  H  A  H  L  A
241  TGCACCCGAGCTGCTGCTGGCCGTGCTCTGCGCTCTGGGGTGGACAGCGTTGCGCTGGGC   300
      A  P  E  L  L  L  A  V  L  C  A  L  G  W  T  A  L  R  W  A
301  AGCCACCACACACATCTTTCGGCCCCTGGCCAAGCGGTGTCGTCTGCAGCCTAGAGATGC   360
      A  T  T  H  I  F  R  P  L  A  K  R  C  R  L  Q  P  R  D  A
361  TGCCAGGTTACCTGAGAGCGCCTGGAAGCTTCTGTTCTACTTGGCCTGTTGGAGCTACTG   420
      A  R  L  P  E  S  A  W  K  L  L  F  Y  L  A  C  W  S  Y  C
421  CGCTTACCTGCTCCTGGGCACCAGTTATCCTTTCTTCCATGACCCGCCCTCTGTCTTCTA   480
      A  Y  L  L  L  G  T  S  Y  P  F  F  H  D  P  P  S  V  F  Y
481  TGACTGGAGGTCAGGCATGGCAGTGCCCTGGGACATCGCGGTGGCCTATTTGCTGCAGGG   540
      D  W  R  S  G  M  A  V  P  W  D  I  A  V  A  Y  L  L  Q  G
541  GAGTTTCTACTGCCACTCCATCTATGCCACCGTGTACATGGACAGCTGGCGTAAGGACTC   600
      S  F  Y  C  H  S  I  Y  A  T  V  Y  M  D  S  W  R  K  D  S
601  GGTGGTCATGCTGGTGCATCACGTGGTCACCCTGCTCCTCATTGCCTCTTCCTACGCCTT   660
      V  V  M  L  V  H  H  V  V  T  L  L  L  I  A  S  S  Y  A  F
661  CCGGTACCACAACGTAGGCCTCCTCGTGTTCTTCCTGCATGACGTCAGCGATGTGCAGCT   720
      R  Y  H  N  V  G  L  L  V  F  F  L  H  D  V  S  D  V  Q  L
721  GGAGTTCACAAAACTCAACATCTACTTTAAGGCTAGGGGTGGTGCCTACCATCGCTTGCA   780
      E  F  T  K  L  N  I  Y  F  K  A  R  G  G  A  Y  H  R  L  H
781  TGGGCTGGTGGCCAACCTGGGCTGCCTCAGCTTCTGTTTCTGCTGGTTCTGGTTCCGCCT   840
      G  L  V  A  N  L  G  C  L  S  F  C  F  C  W  F  W  F  R  L
841  CTACTGGTTCCCGCTCAAGGTTCTGTACGCCACTTGCCACTGCAGCCTGCAGTCTGTGCC   900
      Y  W  F  P  L  K  V  L  Y  A  T  C  H  C  S  L  Q  S  V  P
901  TGACATTCCGTACTACTTCTTCTTCAACATTCTGCTGTTGCTCCTGATGGTCATGAACAT   960
      D  I  P  Y  Y  F  F  F  N  I  L  L  L  L  L  M  V  M  N  I
961  CTATTGGTTCCTGTACATTGTGGCTTTCGCAGCCAAGGTGCTGACTGGTCAGATGCGTGA  1020
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      L  E  D  L  R  E  Y  D  T  L  E  A  Q  T  A  K  P  C  K  A
1081  CGAGAAGCCACTGAGGAATGGCCTGGTGAAGGACAAGCTCTTCTGAGTCTCTTGTCCTCA  1140
      E  K  P  L  R  N  G  L  V  K  D  K  L  F
1141  ACTTCAGCCATCCAGGACTCTATCCCATCCTACCTGGGATACTGACTCCGCCCCTGGAGA  1200
1201  CTCGACCCAGTCCCTGGAGGTCTGCTCCCACCCCTGGAGGCCCGGTCCCGCCTTTGGCGG  1260
1261  CATGGCCTCGCCCCTAGGACAAATAGCCCCGCCCTAAGATTCAGGATGCTACCCTTCTCCA  1320
1321  GGGACTCTGGCTGCCAGCAGCTCCGCCTTTCAGATCAATTCTCGACCACCCACCTTGGGA  1380
1381  CTGCCGCCCAGTCCTGCCCTCTGGATCAGTGGGGTCCAGACACGACGCAGTGGGCTCCGCTGA  1440
1441  AAAGCACCCCCGACCTAAGGTCACCGACCCACTGGCCCCAGACGCCAGTGGGTCTGCCATCGTTTTTGCGACCAC  1500
1501  CTCTCTTGGACACCTCCTGGGAGGAAAATGCTCCCTGTCTGCCATCGTTTTTGCGACCAC  1560
         M  L  P  V  C  H  R  F  C  D  H
1561  CTCCTCCTCCTGCTCTTGCTGCCCTCGACGACCCTGGCCCCCGCGGCCAGCATCCATGGGC  1620
      L  L  L  L  L  L  P  S  T  T  L  A  P  A  P  A  S  M  G
1621  CCCGCTGCCGCCCTGCTCCAGGTTCTTGGGCTTCCCGAAGCGCCCCGGAGCGTCCCCACA  1680
      P  A  A  A  L  L  Q  V  L  G  L  P  E  A  P  R  S  V  P  T
1681  CACCGACCTGTGCCTCCTGTCATGTGGCGCCTATTCCGTCGCCGCGCGACCCCCAGGAGGCC  1740
      H  R  P  V  P  P  V  M  W  R  L  F  R  R  R  D  P  Q  E  A
1741  AGAGTGGGACGCCCTCTGCGGCCATGCCACGTGGAGGAACTAGGGGTCGCCGGAAACATT  1800
      R  V  G  R  P  L  R  P  C  H  V  E  E  L  G  V  A  G  N  I
1801  GTGCGCCACATCCCCGACAGCGGTCTGTCCTCCAGGCCCGCACAACCCGCCAGGACCTCG  1860
      V  R  H  I  P  D  S  G  L  S  S  R  P  A  Q  P  A  R  T  S
1861  GGGCTGTGCCCCGAGTGGACAGTCGTCTTTGACCTGTCGAATGTGGAGCCCACAGAGCGC  1920
      G  L  C  P  E  W  T  V  V  F  D  L  S  N  V  E  P  T  E  R
1921  CCAACACGCGCGCGCTTAGAGTTGCGGCTGGAGGCTGAGAGTGAAGATACAGGGGGGTGG  1980
      P  T  R  A  R  L  E  L  R  L  E  A  E  S  E  D  T  G  G  W
1981  GAGCTAAGCGTGGCACTGTGGGCCGACGCAGAGCATCCAGGGCCTGAGCTGCTGCGCGTG  2040
      E  L  S  V  A  L  W  A  D  A  E  H  P  G  P  E  L  L  R  V
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      P  A  P  P  G  V  L  L  R  A  D  L  L  G  T  A  V  A  A  N
2101  GCATCAGTGCCCTGTACTGTGCGCCTGGCGCTGTCACTGCACCCTGGGGCCACTGCAGCC  2160
      A  S  V  P  C  T  V  R  L  A  L  S  L  H  P  G  A  T  A  A
2161  TGTGGGCGCCTGGCTGAGGCCTCCCTGCTGCTGGTGACGCTGGACCCACGCCTGTGTCCC  2220
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      L  P  R  L  R  R  H  T  E  P  R  V  E  V  G  P  V  G  T  C
2281  CGTACCCGACGGTTGCATGTGAGCTTCCGTGAGGTGGGCTGGCACCGTTGGGTGATCGCG  2340
      R  T  R  R  L  H  V  S  F  R  E  V  G  W  H  R  W  V  I  A
2341  CCGCGTGGCTTCCTAGCCAACTTCTGCCAGGGCACGTGCGCACTACCCGAAACGCTGAGG  2400
      P  R  G  F  L  A  N  F  C  Q  G  T  C  A  L  P  E  T  L  R
2401  GGACCGGCGGGCCGCCTGCACTCAACCACGCTGTGCTGCGCGCGCTCATGCACGCAGCT  2460
      G  P  G  G  P  P  A  L  N  H  A  V  L  R  A  L  M  H  A  A
2461  GCTCCCACCCCGGGTGCAGGCTCGCCCCTGCTGCGGCCAGAGCGTCTATCACCCCATCTCC  2520
      A  P  T  P  G  A  G  S  P  C  C  V  P  E  R  L  S  P  I  S
2521  GTGCTCTTCTTCGACAATAGTGACAACGTGGTCCTGCGACACTACGAAGACATGGTGGTG  2580
      V  L  F  F  D  N  S  D  N  V  V  L  R  H  Y  E  D  M  V  V
2581  GATGAGTGTGGCTGCCGTTGACCACCCGGGACACCCTTTCAGGGACCGCCCCACGCAAAA  2640
      D  E  C  G  C  R
2641  GCAGGGACTGTTTGTTCATGTTTTATTGGTGACAAAAAGCTTAAAACAAATTTGACTAAA  2700
2701  AATTAAGTTCC  2711
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```
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 61  CCCGAGCCCATGCCGAGCTACGCGCAGCTAGTGCAGCGCGGCTGGGGCAGCGCGCTGGCG   120
      P  E  P  M  P  S  Y  A  Q  L  V  Q  R  G  W  G  S  A  L  A
121  GCGGCGCGGGGCTGCACGGACTGCGGCTGGGGGCTGGCGCGCCGTGGCCTGGCTGAGCAC   180
      A  A  R  G  C  T  D  C  G  W  G  L  A  R  R  G  L  A  E  H
181  GCGCACCTGGCGCCGCCCGAGCTGCTGCTGCTGGCGCTCGGCGCGCTGGGCTGGACCGCG   240
      A  H  L  A  P  P  E  L  L  L  L  A  L  G  A  L  G  W  T  A
241  CTGCGCTCCGCGGCCACTGCGCGCCTCTTTCGGCCCCTGGCGAAGCGGTGCTGCCTCCAG   300
      L  R  S  A  A  T  A  R  L  F  R  P  L  A  K  R  C  C  L  Q
301  CCCAGAGATGCCGCCAAGATGCCCGAGAGCGCTTGGAAGTTTCTCTTCTACCTGGGCAGC   360
      P  R  D  A  A  K  M  P  E  S  A  W  K  F  L  F  Y  L  G  S
361  TGGAGCTACAGTGCCTACCTGCTGTTTGGCACCGACTACCCCTTCTTCCATGACCCACCA   420
      W  S  Y  S  A  Y  L  L  F  G  T  D  Y  P  F  F  H  D  P  P
421  TCTGTCTTCTACGACTGGACGCCGGGCATGGCAGTGCCACGGGACATTGCAGCCGCCTAC   480
      S  V  F  Y  D  W  T  P  G  M  A  V  P  R  D  I  A  A  A  Y
481  CTGCTCCAGGGAAGCTTCTATGGCCACTCCATCTACGCTACGCTATACATGGACACCTGG   540
      L  L  Q  G  S  F  Y  G  H  S  I  Y  A  T  L  Y  M  D  T  W
541  CGCAAGGACTCGGTGGTCATGCTGCTCCACCACGTGGTCACTCTCATCCTCATCGTCTCC   600
      R  K  D  S  V  V  M  L  L  H  H  V  V  T  L  I  L  I  V  S
601  TCCTACGCCTTCCGGTACCACAATGTGGGCATCGTGCTCTTCCTGCACGATATCAGT     660
      S  Y  A  F  R  Y  H  N  V  G  I  L  V  L  F  L  H  D  I  S
661  GACGTGCAGCTTGAGTTCACCAAGCTCAACATTTACTTCAAGTCCCGCGGCGGCTCCTAC   720
      D  V  Q  L  E  F  T  K  L  N  I  Y  F  K  S  R  G  G  S  Y
721  CATCGGCTGCATGCCTTGGCAGCAGACTTGGGCTGCCTCAGCTTCGGCTTCAGCTGGTTC   780
      H  R  L  H  A  L  A  A  D  L  G  C  L  S  F  G  F  S  W  F
781  TGGTTCCGCCTCTACTGGTTCCCGCTCAAGGTCCTGTATGCCACCAGTCACTGCAGTCTG   840
      W  F  R  L  Y  W  F  P  L  K  V  L  Y  A  T  S  H  C  S  L
841  CGCACGGTGCCTGACATCCCCTTCTACTTCTTCTTCAATGCGCTCCTGCTGCTGCTCACC   900
      R  T  V  P  D  I  P  F  Y  F  F  F  N  A  L  L  L  L  L  T
901  CTTATGAACCTCTACTGGTTCCTGTACATCGTGGCGTTTGCAGCCAAGGTGTTGACAGGC   960
      L  M  N  L  Y  W  F  L  Y  I  V  A  F  A  A  K  V  L  T  G
961  CAGGTGCACGAGCTGAAGGACCTGCGGGAGTATGACACAGCCGAGGCCCAGAGCCTGAAG  1020
      Q  V  H  E  L  K  D  L  R  E  Y  D  T  A  E  A  Q  S  L  K
1021 CCCAGCAAAGCCGAGAAGCCACTGAGGAACGGCCTGGTGAAGGACAAGCGCTTCTGAACC  1080
      P  S  K  A  E  K  P  L  R  N  G  L  V  K  D  K  R  F
1081 CCTCGGCCCCGCCCCCGTGGACCCGGCCCCACCCCGAATACCCCGGCCACGCTCCCCGTC  1140
1141 CTTGGCCGCCCCTCCACCCCCTCCAACTCTGCTCCTCTAGGGCCGCCGCCACCTCCCCTG  1200
1201 GGACCCCGCCCCCTCATCCTGCCTCCATTTCCCGGCCACGCCCCCAGGACCCGCCTGCCCC  1260
1261 TCCGGGGACACCGGCCCCGCCCTCAGCCCACTGGTCCCGGGCCGCCGGACCCTGCGCA  1320
1321 CTCTCTGGTCATCGCCTGGGAGGAAGATGCCACCGCCGCAGCAAGGTCCCTGCGGCCACC  1380
                   M  P  P  P  Q  Q  G  P  C  G  H  H
1381 ACCTCCTCCTCCTCCTGGCCCTGCTGCTGCCCTCGCTGCCCCTGACCCGCGCCCCCGTGC  1440
      L  L  L  L  A  L  L  L  L  P  S  L  P  L  T  R  A  P  V  P
1441 CCCCAGGCCCCAGCCGCCGCCCCTGCTCCAGGCTCTAGGACTGCGCGATGAGCCCCAGGGTG  1500
      P  G  P  A  A  A  L  L  Q  A  L  G  L  R  D  E  P  Q  G  A
1501 CCCCCCAGGCTCCGGCCGGTTCCCCCGGTCATGTGGCGCCTGTTTCGACGCCGGGACCCCC  1560
      P  R  L  R  P  V  P  P  V  M  W  R  L  F  R  R  R  D  P  Q
1561 AGGAGACCAGGTCTGGCTCGCGGCGGACGTCCCCAGGGGTCACCCTGCAACCGTGCCACG  1620
      E  T  R  S  G  S  R  R  T  S  P  G  V  T  L  Q  P  C  H  V
1621 TGGAGGAGCTGGGGGTCGCCGGAAACATCGTGCGCCACATCCCCGGACCGCGGTGCGCCCA  1680
      E  E  L  G  V  A  G  N  I  V  R  H  I  P  D  R  G  A  P  T
1681 CCCGGGGCCTCGGAGCCTGTCTCGGCCGCGGGGCATTGCCCTGAGTGGACAGTCGTCTTCG  1740
      R  A  S  E  P  V  S  A  A  G  H  C  P  E  W  T  V  V  F  D
1741 ACCTGTCGGCTGTGGAACCCGCTGAGCGCCCGAGCCGGAGTCGAGCCCTGGAGCTGCGTTTCG  1800
      L  S  A  V  E  P  A  E  R  P  S  R  A  R  L  E  L  R  F  A
1801 CGGCGGCGGCGGCGGCAGCCCCGGAGGGCGGCTGGGAGCTGAGCGTGGCGCAAGCGGGCC  1860
      A  A  A  A  A  A  P  E  G  G  W  E  L  S  V  A  Q  A  G  Q
1861 AGGGCGCGGGCGCGGACCCCGGGCCGGTGCTGCTCCGCCAGTTGGTGCCCGCCCTGGGGC  1920
      G  A  G  A  D  P  G  P  V  L  L  R  Q  L  V  P  A  L  G  P
1921 CGCCAGTGCGCGCGGAGCTGCTGGGCGCCGCTTGGGCTCGCAACGCCTCATGGCCGCGCA  1980
      P  V  R  A  E  L  L  G  A  A  W  A  R  N  A  S  W  P  R  S
1981 GCCTCCGCCTGGCGCTGGCGCTACGCCCCCGGGCCCTGCCGCCTGCCGCGCCTGGCCG  2040
      L  R  L  A  L  A  L  R  P  R  A  P  A  A  C  A  R  L  A  E
2041 AGGCCTCGCTGCTGCTGGTGACCCTCGACCCGCGCCTGTGCCACCCCCTGGCCCGGCCGC  2100
      A  S  L  L  L  V  T  L  D  P  R  L  C  H  P  L  A  R  P  R
2101 GGCGCGACGCCGAACCCGTGTTGGGCGGGGGGCGGCCCCGGGGGGCGCTTGTCGCGCGGCGGC  2160
      R  D  A  E  P  V  L  G  G  G  P  G  G  A  C  R  A  R  R  L
2161 TGTACGTGAGCTTCCGCGAGGTGGGCTGGCACCGCTGGGTCATCGCGCCGCGCGGCTTCC  2220
      Y  V  S  F  R  E  V  G  W  H  R  W  V  I  A  P  R  G  F  L
2221 TGGCCAACTACTGCCAGGGTCAGTGCGGCGTGCCCGTCGCGCGCTGTCGGGGTCCGGGGGGC  2280
      A  N  Y  C  Q  G  Q  C  A  L  P  V  A  L  S  G  S  G  G  P
2281 CGCCGGCGCTCAACCACGCTGTGCTGCGCGCGCTCATGCACGCGGCCGCCCCGGGAGCCG  2340
      P  A  L  N  H  A  V  L  R  A  L  M  H  A  A  A  P  G  A  A
2341 CCGACCTGCCCTGCTGCGTGCCCGCGCGCCTGTCGCCCATCTCCGTGCTCTTCTTTGACA  2400
      D  L  P  C  C  V  P  A  R  L  S  P  I  S  V  L  F  F  D  N
2401 ACAGCGACAACGTGGTGCTGCGGCAGTATGAGGACATGGTGGTGGACGAGTGCGGCTGCC  2460
      S  D  N  V  V  L  R  Q  Y  E  D  M  V  V  D  E  C  G  C  R
2461 GCTAACCCGGGGCGGGCAGGGACGCGGGCCCAACAATAAATGCCGCGTGG    2510
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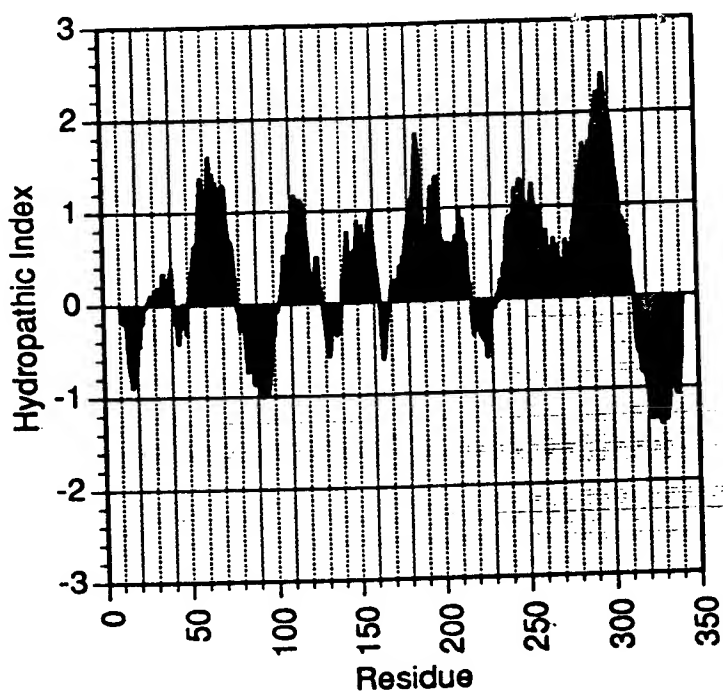
Fig 12

```
          1                                                              57
mGDF-1   MLPVCHRFCDH--LLLL-LLLPSTTLAPAPASMGPAAALLQVLGLPEAPRSVPTHRPVPP
         | |       | |   |||| ||||||   |   ||    ||||||||| |||   |    |   |||||
hGDF-1   MPPPQQGPCGHHLLLLLLALLLPSLPLTRAPVPPGPAAALLQALGLRDEPQGAPRLRPVPP
          1                                                              60

          58                                                            110
mGDF-1    VMWRLFRRRDPQEARVG-R---P---LRPCHVEELGVAGNIVRHIPDSGLSSRPAQPART
          ||||||||||||| | |   |       |   |||||||||||||||||||||| |    |    |
hGDF-1    VMWRLFRRRDPQETRSGSRRTSPGVTLQPCHVEELGVAGNIVRHIPDRGAPTRASEPVSA
          61                                                            120

          111                                                 [S]       166
mGDF-1    SGLCPEWTVVFDLSNVEPTERPTRARLELRLEAPCEDT--GGWELSVALWAD-AE-HPGP
          | |||||||||||| |||  |||  ||||||||  |             |||||||||  |    ||| 
hGDF-1    AGHCPEWTVVFDLSAVEPAERPSRARLELRFAAAAAAAPEGGWELSVAQAGQGAGADPGP
          121                                                           180

          167                                                           225
mGDF-1    ELLRVPAPP-GVLLRADLLGTAVAANASVPCTVRLALSLHPGATAACGRLAEASLLLVTL
          |||    |   |    || |||  || |||   ||||  |  |  |||  ||||||||||||
hGDF-1    VLLRQLVPALGPPVRAELLGAAWARNASWPRSLRLALALRPRAPAACARLAEASLLLVTL
          181                                                           240

          226                                                           284
mGDF-1    DPRLC-PLPRL[RF]HTEPRVEVGPVGTRTRRLHVSFREVGWHRWVIAPRGFLANFOGT
          |||||   |||||| |   || |  || || |  ||| |||||||||||||||||||||||||||
hGDF-1    DPRLCHPLARP[RR]DAEPVLGGGPGGARARRLYVSFREVGWHRWVIAPRGFLANYOGO
          241                                                           300

          285                                                           344
mGDF-1    ALPETLRGPGGPPALNHAVLRALMHAAAPTPGAGSPVPERLSPISVLFFDNSDNVVLR
          |||    | |  |||||||||||||||||||||||||   |  || |||||||||||||||||||
hGDF-1    ALPVALSGSGGPPALNHAVLRALMHAAAPGA-ADLPVPARLSPISVLFFDNSDNVVLR
          301                                                           359

          345      357
mGDF-1    HYEDMVVDEGGR
          |||||||| || |
hGDF-1    QYEDMVVDEGGR
          360      372
```

Fig 13a

```
              1                                                          60
mUOG-1   MAAAAATPRLEAPEPMPSYAQMLQRSWASALAAAQGCGDCGWGLARRGLAEHAHLAAPEL
         ||||       ||||||||||  ||  |  |||||  ||   |||||||||||||||||  |||
hUOG-1   MAAAGPAAGPTGPEPMPSYAQLVQRGWGSALAAARGCTDCGWGLARRGLAEHAHLAPPEL
              1                                                          6C

              61                                                         120
mUOG-1   LLAVLCALGWTALRWAATTHIFRPLAKRCRLQPRDAARLPESAWKLLFYLACWSYCAYLL
         ||   |   ||||||||  |||   |:||||||||| ||||||| ||||||  |||   ||||
hUOG-I   LLLALGALGWTALRSAATARLFRPLAKRCCLQPRDAAKMPESAWKFLFYLGSWSYSAYLL
              61                                                         120

              121                                                        180
mUOG-1   LGTSYPFFHDPPSVFYDWRSGMAVPWDIAVAYLLQGSFYCHSIYATVYMDSWRKDSVVML
         ||  |||||||||||||||||||  |||||  |||  ||||||||||  ||||||  ||||||
hUOG-1   FGTDYPFFHDPPSVFYDWTPGMAVPRDIAAAYLLQGSFYGHSIYATLYMDTWRKDSVVML
              121                                                        180

              181                                                        240
mUOG-1   VHHVVTLLLIASSYAFRYHNVGLLVFFLHDVSDVQLEFTKLNIYFKARGGAYHRLHGLVA
         ||||||  ||  |||||||||||||||||  ||||  ||||||||||||||||||  |||  |||| | |
hUOG-1   LHHVVTLILIVSSYAFRYHNVGILVLFLHDISDVQLEFTKLNIYFKSRGGSYHRLHALAA
              181                                                        240

              241                                                        300
mUOG-1   NLGCLSFCFCWFWFRLYWFPLKVLYATCHCSLQSVPDIPYYFFFNILLLLLMVMNIYWFL
         ||||||| |  ||||||||||||||||||||||  ||||   ||||| |||||| |||||  |||||||
hUOG-1   DLGCLSFGFSWFWFRLYWFPLKVLYATSHCSLRTVPDIPFYFFFNALLLLLTLMNLYWFL
              241                                                        300

              301                                            350
mUOG-1   YIVAFAAKVLTGQMRELEDLREYDTLEAQTAKPCKAEKPLRNGLVKDKLF
         ||||||||||||||  ||  |||||||  |||   || ||||||||||||||| |
hUOG-1   YIVAFAAKVLTGQVHELKDLREYDTAEAQSLKPSKAEKPLRNGLVKDKRF
              301                                            350
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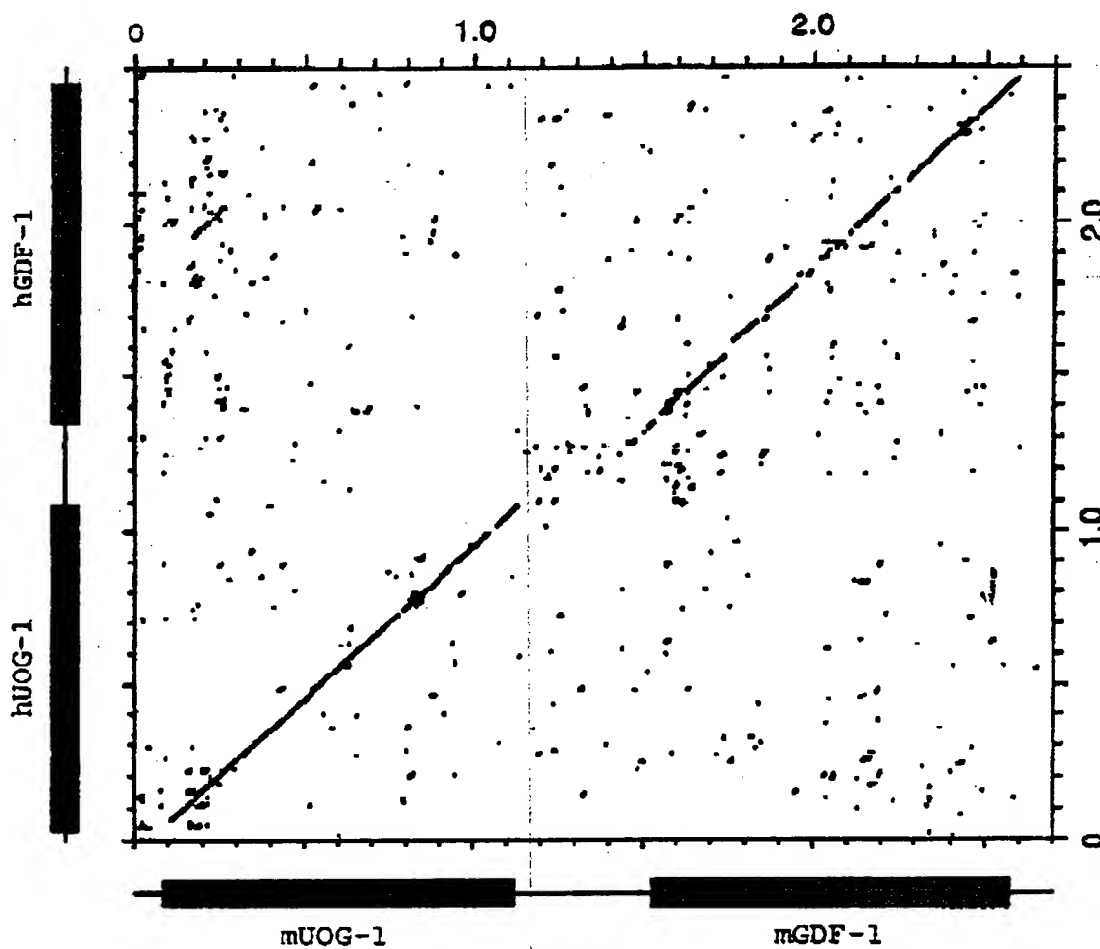
Fig 13b

Fig 13c

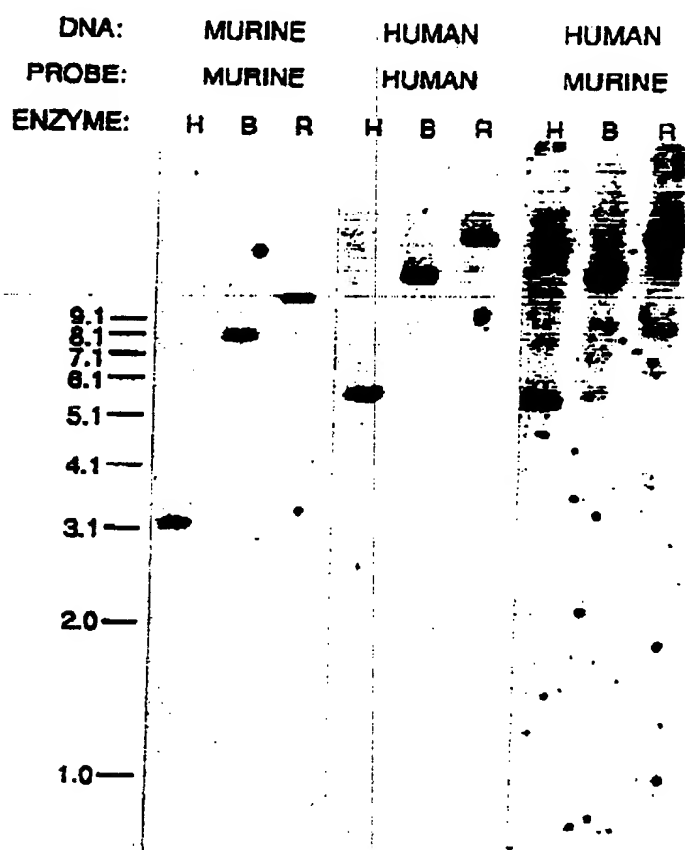Fig 14